

INPUT SET: S35468.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENT

3 (1) General Information:

4

5 (i) APPLICANTS: Jolly, Douglas J.
6 Chang, Stephen M.W.

7 Respess, James G.

8 DePolo, Nicholas J.

9 Hsu, David Chi-Tang

10 Ibanez, Carlos E.

11 Greengard, Judith

12 Lee, Will

13

14 (ii) TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
15 RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
16 OF HEMOPHILIA AND OTHER DISORDERS

17

18 (iii) NUMBER OF SEQUENCES: 84

19

20 (iv) CORRESPONDENCE ADDRESS:
21 (A) ADDRESSEE: Seed Intellectual Property Law Group
22 (B) STREET: 701 Fifth Avenue, Suite 6300
23 (C) CITY: Seattle
24 (D) STATE: Washington
25 (E) COUNTRY: U.S.A.
26 (F) ZIP: 98104

27

28 (v) COMPUTER READABLE FORM:
29 (A) MEDIUM TYPE: Floppy disk
30 (B) COMPUTER: IBM PC compatible
31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

33

34 (vi) CURRENT APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 09/001,039
36 (B) FILING DATE: 13-JAN-1998
37 (C) CLASSIFICATION:

38

39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: McMasters, David D.
41 (B) REGISTRATION NUMBER: 33,963
42 (C) REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C

43

44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (206) 622-4900
46 (B) TELEFAX: (206) 682-6031

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PATENT APPLICATION US/09/001,039B**DATE: 05/11/2000
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47
48
49
50 (2) INFORMATION FOR SEQ ID NO:1:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 24 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: DNA (genomic)
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58 GAGAGATGGG GGAGGCTAAC TGAG 24
59
60 (2) INFORMATION FOR SEQ ID NO:2:
61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 28 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear
66 (ii) MOLECULE TYPE: DNA (genomic)
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
68 GATCCTCAGT TAGCCTCCCC CATCTCTC 28
69
70 (2) INFORMATION FOR SEQ ID NO:3:
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 35 base pairs
73 (B) TYPE: nucleic acid
74 (C) STRANDEDNESS: single
75 (D) TOPOLOGY: linear
76 (ii) MOLECULE TYPE: DNA (genomic)
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
78 TATATCTCCA GATGAGGTAC ATGATTTAG GCTTG 35
79
80 (2) INFORMATION FOR SEQ ID NO:4:
81 (i) SEQUENCE CHARACTERISTICS:
82 (A) LENGTH: 40 base pairs
83 (B) TYPE: nucleic acid
84 (C) STRANDEDNESS: single
85 (D) TOPOLOGY: linear
86 (ii) MOLECULE TYPE: DNA (genomic)
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
88 TATATATCGA TTCAAGGCAT TTTCTTTCA TCAATAAAAC 40
89
90 (2) INFORMATION FOR SEQ ID NO:5:
91 (i) SEQUENCE CHARACTERISTICS:
92 (A) LENGTH: 37 base pairs
93 (B) TYPE: nucleic acid
94 (C) STRANDEDNESS: single
95 (D) TOPOLOGY: linear
96 (ii) MOLECULE TYPE: DNA (genomic)
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
98 TCGAGGATCC GCCCGGGCGG CCGCATCGAT GTCGACG 37
99

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100 (2) INFORMATION FOR SEQ ID NO:6:
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 35 base pairs
103 (B) TYPE: nucleic acid
104 (C) STRANDEDNESS: single
105 (D) TOPOLOGY: linear
106 (ii) MOLECULE TYPE: DNA (genomic)
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
108 CGCGTCGACA TCGATGCGGC CGCCCGGGCG GATCC 35
109
110
111 (2) INFORMATION FOR SEQ ID NO:7:
112 (i) SEQUENCE CHARACTERISTICS:
113 (A) LENGTH: 77 base pairs
114 (B) TYPE: nucleic acid
115 (C) STRANDEDNESS: single
116 (D) TOPOLOGY: linear
117 (ii) MOLECULE TYPE: DNA (genomic)
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
119 AGTGAATTCTG AGCTCGGTAC CCGGGGATCC TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT 60
120 GGCGTACTCA TGGTCAT 77
121
122 (2) INFORMATION FOR SEQ ID NO:8:
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 8 amino acids
125 (B) TYPE: amino acid
126 (C) STRANDEDNESS: single
127 (D) TOPOLOGY: linear
128 (ii) MOLECULE TYPE: protein
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
130 Ala Arg Glu Met Gly Glu Ala Asn
131 1 5
132
133 (2) INFORMATION FOR SEQ ID NO:9:
134 (i) SEQUENCE CHARACTERISTICS:
135 (A) LENGTH: 27 base pairs
136 (B) TYPE: nucleic acid
137 (C) STRANDEDNESS: single
138 (D) TOPOLOGY: linear
139 (ii) MOLECULE TYPE: DNA (genomic)
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
141 CCCGAGAGAT GGGGGAGGGCT AACTGAG 27
142
143 (2) INFORMATION FOR SEQ ID NO:10:
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 31 base pairs
146 (B) TYPE: nucleic acid
147 (C) STRANDEDNESS: single
148 (D) TOPOLOGY: linear
149 (ii) MOLECULE TYPE: DNA (genomic)
150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
151 GGGCTCTCTA CCCCCCTCCGA TTGACACACCA G 31
152

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153 (2) INFORMATION FOR SEQ ID NO:11:
154 (i) SEQUENCE CHARACTERISTICS:
155 (A) LENGTH: 5 amino acids
156 (B) TYPE: amino acid
157 (C) STRANDEDNESS: single
158 (D) TOPOLOGY: linear
159 (ii) MOLECULE TYPE: protein
160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
161 Thr Ile Met Thr Met
162 1 5
163
164
165 (2) INFORMATION FOR SEQ ID NO:12:
166 (i) SEQUENCE CHARACTERISTICS:
167 (A) LENGTH: 24 base pairs
168 (B) TYPE: nucleic acid
169 (C) STRANDEDNESS: single
170 (D) TOPOLOGY: linear
171 (ii) MOLECULE TYPE: DNA (genomic)
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
173 CCCTGTGCCT TATTGAACT AACC 24
174
175 (2) INFORMATION FOR SEQ ID NO:13:
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 24 base pairs
178 (B) TYPE: nucleic acid
179 (C) STRANDEDNESS: single
180 (D) TOPOLOGY: linear
181 (ii) MOLECULE TYPE: DNA (genomic)
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
183 CCCACCAACAA CCACATATCC CTCC 24
184
185 (2) INFORMATION FOR SEQ ID NO:14:
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 19 base pairs
188 (B) TYPE: nucleic acid
189 (C) STRANDEDNESS: single
190 (D) TOPOLOGY: linear
191 (ii) MOLECULE TYPE: DNA (genomic)
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
193 CCAGTCCTCC GATTGACTG 19
194
195 (2) INFORMATION FOR SEQ ID NO:15:
196 (i) SEQUENCE CHARACTERISTICS:
197 (A) LENGTH: 8332 base pairs
198 (B) TYPE: nucleic acid
199 (C) STRANDEDNESS: single
200 (D) TOPOLOGY: linear
201 (ii) MOLECULE TYPE: DNA (genomic)
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
203
204 GCGCCAGTCC TCCGATTGAC TGAGTCGCC GGGTACCCGT GTATCCAATA AACCCCTTTG 60
205

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206	CAGTTGCATC CGACTTGTGG TCTCGCTGTT CCTTGGGAGG GTCTCCTCTG AGTGATTGAC	120
207	TACCCGTCAG CGGGGGTCTT TCATTTGGGG GCTCGTCCGG GATCGGGAGA CCCCTGCCA	180
208	GGGACCACCG ACCCACCACC GGGAGGTAAG CTGGCCAGCA ACTTATCTGT GTCTGTCCGA	240
209	TTGTCTAGTG TCTATGACTG ATTTTATGCG CCTGCGTCGG TACTAGTTAG CTAACTAGCT	300
210	CTGTATCTGG CGGACCCGTG GTGGAACTGA CGAGTTCGGA ACACCCGGCC GCAACCCCTGG	360
211	GAGACGTCCC AGGGACTTCG GGGGCCGTTT TTGTGGCCCG ACCTGAGTCC AAAAATCCCG	420
212	ATCGTTTGG ACTCTTTGGT GCACCCCCCT TAGAGGAGGG ATATGTGGTT CTGGTAGGAG	480
213	ACGAGAACCT AAAACAGTTC CCGCCTCCGT CTGAATTTT GCTTCGGTT TGGGACCGAA	540
214	GCCGCGCCGC GCGTCTTGTG TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT CTGACTGTGT	600
215	TTCTGTATTT GTCTGAGAAT ATGGGCCAGA CTGTTACCAC TCCCTTAAGT TTGACCTTAG	660
216	GTCACTGGAA AGATGTCGAG CGGATCGCTC ACAACCAGTC GGTAGATGTC AAGAAGAGAC	720
217	GTTGGGTTAC CTTCTGCTCT GCAGAAATGGC CAACCTTAA CGTCGGATGG CCGCGAGACG	780
218	GCACCTTAA CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTCA CCTGGCCCGC	840
219	ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT TTTGACCCCC	900
220	CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC TCCTCTTCCT CCATCCGCC	960
221	CGTCTCTCCC CCTTGAAACCT CCTCGTTCGA CCCCGCCTCG ATCCTCCCTT TATCCAGCCC	1020
222	TCACTCCTTC TCTAGGCGCC AAACCTAAAC CTCAAGTTCT TTCTGACAGT GGGGGGCCGC	1080
223	TCATCGACCT ACTTACAGAA GACCCCCGC CTTATAGGGA CCCAAGACCA CCCCCCTTCCG	1140
224	ACAGGGACGG AAATGGTGGA GAAGCGACCC CTGCGGGAGA GGCACCGGAC CCCTCCCCAA	1200
225	TGGCATCTCG CCTACGTGGG AGACGGGAGC CCCCTGTGGC CGACTCCACT ACCTCGCAGG	1260
226	CATTCCCCCT CCGCGCAGGA GGAAACGGAC AGCTTCAATA CTGGCCGTT TCCTCTTCTG	1320
227	ACCTTACAA CTGGAAAAAT AATAACCCTT CTTTTCTGA AGATCCAGGT AACTGACAG	1380
228	CTCTGATCGA GTCTGTTCTC ATCACCCATC AGCCCACCTG GGACGACTGT CAGCAGCTGT	1440
229	TGGGGACTCT GCTGACCGGA GAAGAAAAAC AACGGGTGCT CTTAGAGGCT AGAAAGGCGG	1500
230	TGCGGGGCGA TGATGGCGC CCCACTCAAC TGCCCAATGA AGTCGATGCC GCTTTCCCC	1560
231	TCGAGCGCCC AGACTGGGAT TACACCACCC AGGCAGGTAG GAACCACCTA GTCCACTATC	1620
232	GCCAGTTGCT CCTAGCGGGT CTCCAAAACG CGGGCAGAAG CCCCCACCAAT TTGGCCAAGG	1680

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